



SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: SHEEN, JEN
- (ii) TITLE OF THE INVENTION: STRESS PROTECTED TRANSGENIC PLANTS
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Clark & Elbing LLP
 - (B) STREET: 176 Federal Street
 - (C) CITY: Boston
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02110
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/989,881
 - (B) FILING DATE: 12-DEC-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 60/032,966
 - (B) FILING DATE: 13-DEC-1996
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Elbing, Karen L
 - (B) REGISTRATION NUMBER: 35,238
 - (C) REFERENCE/DOCKET NUMBER: 08472/716002
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 617-428-0200
 - (B) TELEFAX: 617-428-7045
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1020 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
- (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 97...918
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

60	ATTGGAGCTC																60
114	CAG																114
	Met Ala Asn Gln Thr Gln																
	1 5																
162	TTC																162
	Phe																
	10 15 20																
210	GCT																210
	Ala																
	25 30 35																
258	GAA																258
	Glu																
	40 45 50																
306	CCA																306
	Pro																
	60 65 70																
354	CAT																354
	His																
	75 80 85																
402	GTT																402
	Val																
	90 95 100																
450	ACG																450
	Thr																
	105 110 115																
498	AGA																498
	Arg																
	120 125 130																
546	TCT																546
	Ser																
	135 140 145																
594	GGA																594
	Gly																
	155 160 165																
642	GAA																642
	Glu																
	170 175 180																
690	GGA																690
	Gly																
	185 190 195																
738	GAG																738
	Glu																
	200 205 210																
786	TTT																786
	Phe																
	215 220 225																
834	GTG																834
	Val																
	235 240 245																



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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 97...918
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTTGTAAAC	GACGGNCAGT	GAATTGTAAT	ACGACTCNCT	ATAGGGCGNA	ATTGGAGCTC	60
CACCGCGGTG	GCGGCCGCTC	TAGAACTAGT	GGATCC	ATG GCT AAT CAA ACT CAG	114	
				Met Ala Asn Gln Thr Gln		
				1 5		
ATC AGC GAC AAG TAC ATC TTA GGA CGA GAA CTC GGT CGC GGC GAA TTC	162					
Ile Ser Asp Lys Tyr Ile Leu Gly Arg Glu Leu Gly Arg Gly Glu Phe						
10 15 20						
GGA ATC ACG TAT CTT TGT ACA GAT AGA GAG ACT CGT GAA GCT TTA GCT	210					
Gly Ile Thr Tyr Leu Cys Thr Asp Arg Glu Thr Arg Glu Ala Leu Ala						
25 30 35						
TGC AAA TCA ATC TCC AAG AGA AAG CTC CGA ACC GCC GTC GAT GTG GAA	258					
Cys Lys Ser Ile Ser Lys Arg Lys Leu Arg Thr Ala Val Asp Val Glu						
40 45 50						
GAC GTC CGT CGT GAA GTC ACG ATC ATG TCA ACT TTA CCG GAA CAC CCA	306					
Asp Val Arg Arg Glu Val Thr Ile Met Ser Thr Leu Pro Glu His Pro						
55 60 65 70						
AAC GTT GTG AAA CTT AAA GCG ACT TAT GAG GAT AAC GAG ACC GTG CAT	354					
Asn Val Val Lys Leu Lys Ala Thr Tyr Glu Asp Asn Glu Thr Val His						
75 80 85						
CTT GTG ATG GAG CTT TGT GAA GGA GGT GAG CTT TTT GGT CGG ATT GTT	402					
Leu Val Met Glu Leu Cys Glu Gly Gly Glu Leu Phe Gly Arg Ile Val						
90 95 100						
GCA AGA GGA CAT TAT ACA GAG CGT GCG GCG GCT ACC GTC GCG AGA ACG	450					
Ala Arg Gly His Tyr Thr Glu Arg Ala Ala Ala Thr Val Ala Arg Thr						
105 110 115						
ATC GCG GAA GTT GTG AGG ATG TGT CAT GTC AAT GGT GTT ATG CAT AGA	498					
Ile Ala Glu Val Val Arg Met Cys His Val Asn Gly Val Met His Arg						

120	125	130	
GAT TTG AAG CCT GAG AAT TTC TTG TTT GCT AAC AAG AAG GAG AAT TCT			546
Asp Leu Lys Pro Glu Asn Phe Leu Phe Ala Asn Lys Lys Glu Asn Ser			
135	140	145	150
GCA CTT AAG GCT ATT GAT TTT GGT TTA TCT GTT CTC TTT AAA CCT GGA			594
Ala Leu Lys Ala Ile Asp Phe Gly Leu Ser Val Leu Phe Lys Pro Gly			
	155	160	165
GAG AGG TTT ACA GAG ATT GTT GGA AGT CCT TAT TAT ATG GCT CCA GAA			642
Glu Arg Phe Thr Glu Ile Val Gly Ser Pro Tyr Tyr Met Ala Pro Glu			
	170	175	180
GTG TTG AAG AGA AAT TAT GGA CCA GAG GTT GAT GTG TGG AGT GCT GGA			690
Val Leu Lys Arg Asn Tyr Gly Pro Glu Val Asp Val Trp Ser Ala Gly			
	185	190	195
GTT ATC CTC TAC ATC TTG CTT TGT GGT GTT CCT CCG TTT TGG GCA GAG			738
Val Ile Leu Tyr Ile Leu Leu Cys Gly Val Pro Pro Phe Trp Ala Glu			
	200	205	210
ACT GAA CAA GGT GTG GCT CTT GCC ATC TTG AGG GGA GTT CTT GAT TTT			786
Thr Glu Gln Gly Val Ala Leu Ala Ile Leu Arg Gly Val Leu Asp Phe			
	215	220	225
AAG AGA GAT CCT TGG TCG CAG ATA TCA GAG AGC GCA AAG AGC CTT GTG			834
Lys Arg Asp Pro Trp Ser Gln Ile Ser Glu Ser Ala Lys Ser Leu Val			
	235	240	245
AAG CAG ATG TTG GAA CCT GAT TCA ACT AAG CGT TTG ACT GCT CAG CAA			882
Lys Gln Met Leu Glu Pro Asp Ser Thr Lys Arg Leu Thr Ala Gln Gln			
	250	255	260
GTT CTT GAT CAC CCT TGG ATA CAG AAT GCA AAG AAA AGGATCAAGC TTATCG			934
Val Leu Asp His Pro Trp Ile Gln Asn Ala Lys Lys			
	265	270	
ATACCGTCGA CCTCGAGGGG GGGCCCGGTA CCAGCTTTNG TTCCCTTTAG TGAGGGTTAA			994
TTTCGAGCTT GCGTAATCA TGTCAT			1020

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Asn Gln Thr Gln Ile Ser Asp Lys Tyr Ile Leu Gly Arg Glu
1 5 10 15
Leu Gly Arg Gly Glu Phe Gly Ile Thr Tyr Leu Cys Thr Asp Arg Glu
20 25 30
Thr Arg Glu Ala Leu Ala Cys Lys Ser Ile Ser Lys Arg Lys Leu Arg
35 40 45
Thr Ala Val Asp Val Glu Asp Val Arg Arg Glu Val Thr Ile Met Ser
50 55 60
Thr Leu Pro Glu His Pro Asn Val Val Lys Leu Lys Ala Thr Tyr Glu
65 70 75 80
Asp Asn Glu Thr Val His Leu Val Met Glu Leu Cys Glu Gly Gly Glu
85 90 95
Leu Phe Gly Arg Ile Val Ala Arg Gly His Tyr Thr Glu Arg Ala Ala
100 105 110
Ala Thr Val Ala Arg Thr Ile Ala Glu Val Val Arg Met Cys His Val
115 120 125
Asn Gly Val Met His Arg Asp Leu Lys Pro Glu Asn Phe Leu Phe Ala
130 135 140
Asn Lys Lys Glu Asn Ser Ala Leu Lys Ala Ile Asp Phe Gly Leu Ser
145 150 155 160
Val Leu Phe Lys Pro Gly Glu Arg Phe Thr Glu Ile Val Gly Ser Pro
165 170 175
Tyr Tyr Met Ala Pro Glu Val Leu Lys Arg Asn Tyr Gly Pro Glu Val
180 185 190
Asp Val Trp Ser Ala Gly Val Ile Leu Tyr Ile Leu Leu Cys Gly Val
195 200 205
Pro Pro Phe Trp Ala Glu Thr Glu Gln Gly Val Ala Leu Ala Ile Leu
210 215 220
Arg Gly Val Leu Asp Phe Lys Arg Asp Pro Trp Ser Gln Ile Ser Glu
225 230 235 240
Ser Ala Lys Ser Leu Val Lys Gln Met Leu Glu Pro Asp Ser Thr Lys
245 250 255
Arg Leu Thr Ala Gln Gln Val Leu Asp His Pro Trp Ile Gln Asn Ala
260 265 270
Lys Lys